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#2

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          RAW SEQUENCE LISTING              DATE: 10/04/2001
          PATENT APPLICATION:  US/09/950,071   TIME: 10:31:45

          Input Set : A:\212532US0.txt
          Output Set: N:\CRF3\10042001\I950071.raw
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   3 <110> APPLICANT: FARWICK, Mike
   4        HUTHMACHER, Klaus
   5        PFEFFERLE, Walter
   6        BATHE, Brigitte
   8 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE RODA PROTEIN
  10 <130> FILE REFERENCE: 212532US0
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/950,071
C--> 12 <141> CURRENT FILING DATE: 2001-09-12
  12 <150> PRIOR APPLICATION NUMBER: DE10044943.3
  13 <151> PRIOR FILING DATE: 2000-09-12
  15 <150> PRIOR APPLICATION NUMBER: DE10132947.4
  16 <151> PRIOR FILING DATE: 2001-07-06
  18 <160> NUMBER OF SEQ ID NOS: 4
  20 <170> SOFTWARE: PatentIn version 3.1
  22 <210> SEQ ID NO: 1
  23 <211> LENGTH: 1761
  24 <212> TYPE: DNA
  25 <213> ORGANISM: Corynebacterium glutamicum
  27 <220> FEATURE:
  28 <221> NAME/KEY: CDS
  29 <222> LOCATION: (238)..(1560)
  30 <223> OTHER INFORMATION:
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  36 ggatgattta ccggcatctg ttcgcggtag tgtcgcagga ttaccgtctg ggtcgtatga   120
  38 cgaggtccag gcgcaaatgc aacggctggc tgctcaagct ttgccagtgt gcgtgaactt   180
  40 agaagtaaca accggtggcg atagaaacga acccggagtc aattgtaggg aggtctc      237
  42 atg aac acg ctt gaa cga tta aag ctt cgt cgc acg gaa atg tgg ctg      285
  43 Met Asn Thr Leu Glu Arg Leu Lys Leu Arg Arg Thr Glu Met Trp Leu
  44 1               5                   10                  15
  46 ctg ata ctt gcc aca ctc gtt gtg tcg atc atg ttc atc agc ctc gag      333
  47 Leu Ile Leu Ala Thr Leu Val Val Ser Ile Met Phe Ile Ser Leu Glu
  48             20                  25                  30
  50 ctg gcc atg ggc aat gag ttg ggt acc cat att ttg atg ctg atg ggc      381
  51 Leu Ala Met Gly Asn Glu Leu Gly Thr His Ile Leu Met Leu Met Gly
  52          35                  40                  45
  54 gga tat atc ggt atc ttc atc gtc gcg cac cta gcc atg gca tgg gtg      429
  55 Gly Tyr Ile Gly Ile Phe Ile Val Ala His Leu Ala Met Ala Trp Val
  56      50                  55                  60
  58 gcg ccg ttt gct gat caa atc atg ctg cct gtg gtg gcg gtg ctc aat      477
  59 Ala Pro Phe Ala Asp Gln Ile Met Leu Pro Val Val Ala Val Leu Asn
  60 65                  70                  75                  80
  62 ggc att ggt ttg gtg atg att tat cgc ctt gat gag gcc acg ggc tac      525
  63 Gly Ile Gly Leu Val Met Ile Tyr Arg Leu Asp Glu Ala Thr Gly Tyr
  64              85                  90                  95
  66 agc acg gtc aat agc caa ttg atg tgg acg gtt gtt ggc gtc acg ctg      573
  67 Ser Thr Val Asn Ser Gln Leu Met Trp Thr Val Val Gly Val Thr Leu
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70 atg gtg gct gtg ttg ttg ctg ttg cgt gat tac aag tcg ctt tcg cgt       621
71 Met Val Ala Val Leu Leu Leu Leu Arg Asp Tyr Lys Ser Leu Ser Arg
72          115               120               125
74 tat tcc tac ctc ctc ggt gtg gtg ggc atc gtg ctg ctg gcg ctg cct       669
75 Tyr Ser Tyr Leu Leu Gly Val Val Gly Ile Val Leu Leu Ala Leu Pro
76     130               135               140
78 ctc gtg tgg ccg cag cca ggc ggc gtg gaa gcc cgc atc tgg att tgg       717
79 Leu Val Trp Pro Gln Pro Gly Gly Val Glu Ala Arg Ile Trp Ile Trp
80 145               150               155               160
82 ctt gga cct ttc tcc atc cag cca ggt gag ttc tcc aag att ttg ctg       765
83 Leu Gly Pro Phe Ser Ile Gln Pro Gly Glu Phe Ser Lys Ile Leu Leu
84               165               170               175
86 ctg ctg ttc ttt gct cag ctg cta gcc acc aag cgt gct ttg ttt act       813
87 Leu Leu Phe Phe Ala Gln Leu Leu Ala Thr Lys Arg Ala Leu Phe Thr
88          180               185               190
90 gtt gcg ggc tac cgt ttc ctc ggc atg gat ttc cct cgt ttg cgt gac       861
91 Val Ala Gly Tyr Arg Phe Leu Gly Met Asp Phe Pro Arg Leu Arg Asp
92          195               200               205
94 ctc gcg ccg att ctt gtg gtg tgg gcg ttg gct att ttg atc atg gct       909
95 Leu Ala Pro Ile Leu Val Val Trp Ala Leu Ala Ile Leu Ile Met Ala
96     210               215               220
98 ggc gcc aac gac ttc ggt cct gca ctg ctg ctt ttc act acc gtt ttg       957
99 Gly Ala Asn Asp Phe Gly Pro Ala Leu Leu Leu Phe Thr Thr Val Leu
100 225               230               235               240
102 gcc atg gtg tac ctg gct acc ggc cgt ggt tcc tgg ctg ttg att ggt      1005
103 Ala Met Val Tyr Leu Ala Thr Gly Arg Gly Ser Trp Leu Leu Ile Gly
104               245               250               255
106 gct gtg ttg gtg gct gtc ggc gcg ttc gcg gtg tac caa gtt tca agc      1053
107 Ala Val Leu Val Ala Val Gly Ala Phe Ala Val Tyr Gln Val Ser Ser
108          260               265               270
110 aag att cag gaa cgc gtg caa aac ttc gtg gat cct gtg gcc cac tat      1101
111 Lys Ile Gln Glu Arg Val Gln Asn Phe Val Asp Pro Val Ala His Tyr
112          275               280               285
114 gac acc acc ggt tac cag ctg tcc cag tcc ttg ttt ggc atg agt tgg      1149
115 Asp Thr Thr Gly Tyr Gln Leu Ser Gln Ser Leu Phe Gly Met Ser Trp
116     290               295               300
118 ggc gga atc acc ggc acc ggc att ggt cag ggt tac ccc aac atg atc      1197
119 Gly Gly Ile Thr Gly Thr Gly Ile Gly Gln Gly Tyr Pro Asn Met Ile
120 305               310               315               320
122 cct gtc gtg cac tcg gac ttc att ctc gca gcc att ggt gag gag ctt      1245
123 Pro Val Val His Ser Asp Phe Ile Leu Ala Ala Ile Gly Glu Glu Leu
124               325               330               335
126 ggt ctg att ggc ctg gcg gcc atc atc gtg ctg ttt ggt gtg ttt gtc      1293
127 Gly Leu Ile Gly Leu Ala Ala Ile Ile Val Leu Phe Gly Val Phe Val
128          340               345               350
130 acc cgc ggt atg cgc acc gct acc ctg gct cgt gac agc tac gga aag      1341
131 Thr Arg Gly Met Arg Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys
132          355               360               365
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134 ctc gtg gca tct ggt ctg tcg atg acc atc atg atc cag att ttc gtc      1389
135 Leu Val Ala Ser Gly Leu Ser Met Thr Ile Met Ile Gln Ile Phe Val
136     370             375             380
138 gtc gtg gca ggt att tct tca ctg atg ccc atg aca ggt ttg acc act      1437
139 Val Val Ala Gly Ile Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr
140 385             390             395             400
142 ccg ttt atg tcc cag ggt ggt tca tcc ctg atg gct aac tac att ctg      1485
143 Pro Phe Met Ser Gln Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu
144             405             410             415
146 atg gcc atc atc ttg cgt att tct gac agt gcc cgc cga cct gtc atg      1533
147 Met Ala Ile Ile Leu Arg Ile Ser Asp Ser Ala Arg Arg Pro Val Met
148             420             425             430
150 tcc aag caa gca tcg gag gtg gct gcg tgaaccgctc gattcgaatc            1580
151 Ser Lys Gln Ala Ser Glu Val Ala Ala
152         435             440
154 acatccctct tctctttgct cctgatcttg gtgctcgtag caaacctcac ctggattcag    1640
156 gcttttaggg acgatgatct tgctcagaac ccactgaacg cacgtggttt cctggaggcg    1700
158 aagtccactc cgcgtggaca gatttcaact ggtggccaag tactcgcaga gtcctcccag    1760
160 g                                                                    1761
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 441
165 <212> TYPE: PRT
166 <213> ORGANISM: Corynebacterium glutamicum
168 <400> SEQUENCE: 2
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175             20              25              30
178 Leu Ala Met Gly Asn Glu Leu Gly Thr His Ile Leu Met Leu Met Gly
179         35              40              45
182 Gly Tyr Ile Gly Ile Phe Ile Val Ala His Leu Ala Met Ala Trp Val
183     50              55              60
186 Ala Pro Phe Ala Asp Gln Ile Met Leu Pro Val Val Ala Val Leu Asn
187 65              70              75              80
190 Gly Ile Gly Leu Val Met Ile Tyr Arg Leu Asp Glu Ala Thr Gly Tyr
191             85              90              95
194 Ser Thr Val Asn Ser Gln Leu Met Trp Thr Val Val Gly Val Thr Leu
195             100             105             110
198 Met Val Ala Val Leu Leu Leu Leu Arg Asp Tyr Lys Ser Leu Ser Arg
199         115             120             125
202 Tyr Ser Tyr Leu Leu Gly Val Val Gly Ile Val Leu Leu Ala Leu Pro
203     130             135             140
206 Leu Val Trp Pro Gln Pro Gly Gly Val Glu Ala Arg Ile Trp Ile Trp
207 145             150             155             160
210 Leu Gly Pro Phe Ser Ile Gln Pro Gly Glu Phe Ser Lys Ile Leu Leu
211             165             170             175
214 Leu Leu Phe Phe Ala Gln Leu Leu Ala Thr Lys Arg Ala Leu Phe Thr
215         180             185             190
218 Val Ala Gly Tyr Arg Phe Leu Gly Met Asp Phe Pro Arg Leu Arg Asp
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219          195                 200                 205
222 Leu Ala Pro Ile Leu Val Val Trp Ala Leu Ala Ile Leu Ile Met Ala
223     210                 215                 220
226 Gly Ala Asn Asp Phe Gly Pro Ala Leu Leu Leu Phe Thr Thr Val Leu
227 225                 230                 235                 240
230 Ala Met Val Tyr Leu Ala Thr Gly Arg Gly Ser Trp Leu Leu Ile Gly
231             245                 250                 255
234 Ala Val Leu Val Ala Val Gly Ala Phe Ala Val Tyr Gln Val Ser Ser
235             260                 265                 270
238 Lys Ile Gln Glu Arg Val Gln Asn Phe Val Asp Pro Val Ala His Tyr
239         275                 280                 285
242 Asp Thr Thr Gly Tyr Gln Leu Ser Gln Ser Leu Phe Gly Met Ser Trp
243     290                 295                 300
246 Gly Gly Ile Thr Gly Thr Gly Ile Gly Gln Gly Tyr Pro Asn Met Ile
247 305                 310                 315                 320
250 Pro Val Val His Ser Asp Phe Ile Leu Ala Ala Ile Gly Glu Glu Leu
251             325                 330                 335
254 Gly Leu Ile Gly Leu Ala Ala Ile Ile Val Leu Phe Gly Val Phe Val
255             340                 345                 350
258 Thr Arg Gly Met Arg Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys
259         355                 360                 365
262 Leu Val Ala Ser Gly Leu Ser Met Thr Ile Met Ile Gln Ile Phe Val
263     370                 375                 380
266 Val Val Ala Gly Ile Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr
267 385                 390                 395                 400
270 Pro Phe Met Ser Gln Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu
271             405                 410                 415
274 Met Ala Ile Ile Leu Arg Ile Ser Asp Ser Ala Arg Arg Pro Val Met
275         420                 425                 430
278 Ser Lys Gln Ala Ser Glu Val Ala Ala
279     435                 440
282 <210> SEQ ID NO: 3
283 <211> LENGTH: 28
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: synthetic DNA
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295 <211> LENGTH: 28
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: synthetic DNA
302 <400> SEQUENCE: 4
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VERIFICATION SUMMARY   DATE: 10/04/2001
PATENT APPLICATION: US/09/950,071   TIME: 10:31:46

Input Set : A:\212532US0.txt
Output Set: N:\CRF3\10042001\I950071.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date